

GenCore version 6.2.1
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OW nucleic - nucleic search, using sw model

Run on: August 6, 2008, 16:09:37 ; Search time 15127 Seconds
(without alignments)
11364.178 Million cell updates/sec

Title: US-10-720-177-1
Perfect score: 2100
Sequence: 1 caccaaatccgcgaatoca.....ttgggattaagtgcctgcag 2100

Scoring table: IDENTITY_NUC ←
Gapop 10.0, Gapext 0.1 ←

Searched: 9598671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_envr:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_in:*
13: gb_on:*
14: gb_ba:*
15: gb_htg1:*
16: gb_htg2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB ID	Description
	1	2100	100.0	2100	CQ817719	CQ817719 Sequence

2	2100	100.0	2100	2	DD028154	DD028154 Method fo
c 3	2018.2	96.1	110000	14	BA000036_26	Continuation (27 o
c 4	2018.2	96.1	349136	14	BX927155	BX927155 Corynebac
c 5	2018.2	96.1	349980	2	AX127151	AX127151 Sequence
c 6	1977.9	94.2	110000	14	AP009044_26	Continuation (27 o
7	1589.1	75.7	1629	2	BD164926	BD164926 Novel pol
8	1589.1	75.7	1629	2	AX122809	AX122809 Sequence
9	1436.1	68.4	1468	2	AX764345	AX764345 Sequence
10	1436.1	68.4	1468	2	EA032755	EA032755 Sequence
c 11	884.2	42.1	110000	14	BA000035_25	Continuation (26 o
12	845	40.2	861	2	DD097361	DD097361 CORYNEBAC
13	845	40.2	861	2	DD097362	DD097362 CORYNEBAC
14	845	40.2	861	2	AX063819	AX063819 Sequence
15	845	40.2	861	2	AX063821	AX063821 Sequence
c 16	415.6	19.8	453	2	BD164925	BD164925 Novel pol
c 17	415.6	19.8	453	2	AX122808	AX122808 Sequence
18	371.1	17.7	1371	14	DQ019448	DQ019448 Micrococ
19	371.1	17.7	1380	2	EL7152	EL7152 Micrococcus
20	303.4	14.4	1395	4	AY702086	AY702086 Aspergill
21	303.4	14.4	110000	4	AP001715_15	Continuation (16 o
c 22	296.7	14.1	110000	14	CP000431_73	Continuation (74 o
23	288.8	13.8	110000	14	CP000656_24	Continuation (25 o
c 24	288.5	13.7	110000	14	CP000781_17	Continuation (18 o
c 25	282.5	13.5	110000	14	BA000040_53	Continuation (54 o
c 26	277.6	13.2	110000	14	BA000040_43	Continuation (44 o
c 27	274	13.0	110000	14	CP000454_44	Continuation (45 o
c 28	263.4	12.5	110000	14	CU234118_33	Continuation (34 o
29	249.1	11.9	110000	14	CP000781_13	Continuation (14 o
30	248.9	11.9	1368	2	AB319163	AB319163 Sequence
c 31	245.5	11.7	110000	14	CP000494_37	Continuation (38 o
32	244.1	11.6	110000	14	CP000521_11	Continuation (12 o
33	234.1	11.1	110000	14	CR543861_10	Continuation (11 o
34	220.1	10.5	110000	14	CP000473_005	Continuation (6 of
35	209.2	10.0	110000	14	CP000474_03	Continuation (4 of
c 36	205.9	9.8	110000	14	CP000325_38	Continuation (39 o
37	203.4	9.7	110000	14	AY171867_00	AY171867 Clavibact
38	196.2	9.3	110000	14	CP000449_31	Continuation (32 o
39	194.8	9.3	110000	14	CP000353_01	Continuation (2 of
40	188.3	9.0	110000	14	CP000117_11	Continuation (12 o
c 41	178.6	8.5	110000	14	CP000473_067	Continuation (68 o
c 42	175.5	8.4	110000	14	BA000019_35	Continuation (36 o
c 43	172.8	8.2	110000	14	CT573326_35	Continuation (36 o
c 44	172.1	8.2	110000	14	BX571966_08	Continuation (9 of
c 45	172.1	8.2	110000	14	CP000011_08	Continuation (9 of

ALIGNMENTS

LOCUS	CQ817719	2100 bp	DNA	linear	PAT 07-JUN-2004
DEFINITION	Sequence 1 from Patent: EP1424397.				
ACCESSION	CQ817719				
VERSION	CQ817719.1	GI:48426722			
KEYWORDS	.				
SOURCE	Brevibacterium flavum				

Qy 1981 CTGCAAGACGAGTGTGACGGTAGCTTTATGCTGGAACATTCGAAGGAGATTATC 2040
 |||
 Db 1981 CTGCAAGACGAGTGTGACGGTAGCTTTATGCTGGAACATTCGAAGGAGATTATC 2040
 |||
 Qy 2041 GGTGAAAAGAGCTTATGTTGCTTTGATTTGAGCTTTGGGATTAAGTCTGCG 2100
 |||
 Db 2041 GGTGAAAAGAGCTTATGTTGCTTTGATTTGAGCTTTGGGATTAAGTCTGCG 2100
 |||

RESULT 3
 BA000036_26/c
 WPC098MT

Sequence split into 33 fragments LOCUS BA000036 Accession BA000036

Fragment Name	Begin	End
BA000036_00	1	110000
BA000036_01	100001	210000
BA000036_02	200001	310000
BA000036_03	300001	410000
BA000036_04	400001	510000
BA000036_05	500001	610000
BA000036_06	600001	710000
BA000036_07	700001	810000
BA000036_08	800001	910000
BA000036_09	900001	1010000
BA000036_10	1000001	1110000
BA000036_11	1100001	1210000
BA000036_12	1200001	1310000
BA000036_13	1300001	1410000
BA000036_14	1400001	1510000
BA000036_15	1500001	1610000
BA000036_16	1600001	1710000
BA000036_17	1700001	1810000
BA000036_18	1800001	1910000
BA000036_19	1900001	2010000
BA000036_20	2000001	2110000
BA000036_21	2100001	2210000
BA000036_22	2200001	2310000
BA000036_23	2300001	2410000
BA000036_24	2400001	2510000
BA000036_25	2500001	2610000
BA000036_26	2600001	2710000
BA000036_27	2700001	2810000
BA000036_28	2800001	2910000
BA000036_29	2900001	3010000
BA000036_30	3000001	3110000
BA000036_31	3100001	3210000
BA000036_32	3200001	3309401

Continuation (21 of 33) of BA000036 from base 2600001 (BA000036 Corynebacterium glutamicum ATCC 13032 DNA, complete genome. 5/2007)

→ Query Match 96.14; Score 2018.2; DB 14; Length 110000;
 Best Local Similarity 97.74; Pred. No. 0;
 Matches 2067; Conservative 0; Mismatches 28; Indels 20; Gaps 3;
 Qy 1 CACAAAATCCGGGAAATCCACGAAATCGTCTTCACTCTTTGGTTGATCAAAATGCTTCA 60
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 Db 28499 CACAAAATCCGGGAAATCCACGAAATCGTCTTCACTCTTTGGTTGATCAAAATGCTTCA 28440
 |||

Qy 61 TCGGCGCGGCTGACGCTGACGCTTGAGAAATAGAAATAGCGCTTGTGAGCGCAACCC 120
 |||
 Db 28439 TCGGCGCGGCTGACGCTGACGCTTGAGAAATAGAAATAGCGCTTGTGAGCGCAACCC-- 28382
 |||
 Qy 121 ACTCTCAAGCGCAACCC-----GCGAGCGGTGGCAATCGCCGAGATTAT 166
 |||
 Db 28381 ---CTCAAGCGCAACCCGCGAGCGCTTGTGAGCGGTGGCAATCGCCGAGATTAT 28325
 |||
 Qy 167 TAGGACCGGGAATAGTAATGAGTGGAGTACCCCTGATCCACAAATGCAACAGCT 226
 |||
 Db 28324 TAGGACCGGGAATAGTAATGAGTGGAGTACCCCTGATCCACAAATGCAACAGCT 28265
 |||
 Qy 227 TCGCGTACGCTGTAGTATTCACACATCAGCTGGGAATACCTTGCATTCACGGTCA 286
 |||
 Db 28264 TCGCGTACGCTGTAGTATTCACACATCAGCTGGGAATACCTTGCATTCACGGTCA 28205
 |||
 Qy 287 TTATACAGTGGGAATTTCCCGCGCATTTTGTGGATCTCACAGAAATCCATCTTGAG 346
 |||
 Db 28204 TTATACAGTGGGAATTTCCCGCGCATTTTGTGGATCTCACAGAAATCCATCTTGAG 28145
 |||
 Qy 347 CAGCGAGCAATAGCCATCGCGTGGGGAGCATCTTGTCCAGCACTCCCTGGACTTA 406
 |||
 Db 28144 CAGCGAGCAATAGCCATCGCGTGGGGAGCATCTTGTCCAGCACTCCCTGGACTTA 28085
 |||
 Qy 407 TCGCGCATCCCGGGGTGCAACAGCGCATAGCCGTAGTCTTGGGCACTGCT 466
 |||
 Db 28084 TCGCGCATCCCGGGGTGCAACAGCGCATAGCCGTAGTCTTGGGCACTGCT 28025
 |||
 Qy 467 GCGCGCTTGGAAATTTCCAGGAAGGGAATCGATCGTGGTGGCAACATAGCA 526
 |||
 Db 28024 GCGCGCTTGGAAATTTCCAGGAAGGGAATCGATCGTGGTGGCAACATAGCA 27965
 |||
 Qy 527 TGATACCGGTGTTTGGCGTGAAGAGCTGAGTTTCCACACGGTTGGGATTTCTCC 586
 |||
 Db 27964 TGATACCGGTGTTTGGCGTGAAGAGCTGAGTTTCCACACGGTTGGGATTTCTCC 27905
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 Qy 587 GCGTGGAAAACTCACTCGCCAGCTGGGAAAGCGCGGAGCAAGTGAAGGGGAG 646
 |||
 Db 27904 GCGTGGAAAACTCACTCGCCAGCTGGGAAAGCGCGGAGCAAGTGAAGGGGAG 27845
 |||
 Qy 647 ACGCGAGCATTTTGGCATCATAAATGGTGGCTTTGAGTGGCTTG-SCCCAGAA 705
 |||
 Db 27844 ACGCGAGCATTTTGGCATCATAAATGGTGGCTTTGAGTGGCTTGAGGCCAGAA 27785
 |||
 Qy 706 TCTGTATGACACAGACTATATGCGCAAAAGAAATCACTAGTCTTGATTTATTTGAC 765
 |||
 Db 27784 TCTGTATGACACAGACTATATGCGCAAAAGAAATCACTAGTCTTGATTTATTTGAC 27725
 |||
 Qy 766 GATGCGAGTACCGGAGTACCTGACGAAATTTAGATGATCGCGGAGCAACCTCCG 825
 |||
 Db 27724 GATGCGAGTACCGGAGTACCTGACGAAATTTAGATGATCGCGGAGCAACCTCCG 27665
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 Qy 826 CGAGTTGGCGATTATACATCCGGAATCAAAATTCGCCGAACCAACCGCTGGAGTAGC 885
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 Db 27664 CGAGTTGGCGATTATACATCCGGAATCAAAATTCGCCGAACCAACCGCTGGAGTAGC 27605
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Qy 886 CCTGTGACCGTTAAGGACACATCTACAGGCGAGGGATGAGCAGATGAATTACACAT 945
 Db 27604 CCTGTGACCGTTAAGGACACATCTACAGGCGAGGGATGAGCAGATGAATTACACAT 27545

Qy 946 GOMAGATTTTCCAGCCCTTTCCTAGCAGCTCGACCTCCAGAGATGCGGCTTGAATGA 1005
 Db 27544 GOMAGATTTTCCAGCATTTCCTAGCAGCTCGACCTCCAGAGATGCGGCTTGAATGA 27485

Qy 1006 GGTCTGTGATTCGGTGGCTTGGAGCCCTCGGTTGAGGCTTTCAGAGAACCTTCCTCGGA 1065
 Db 27484 GGTCTGTGATTCGGTGGCTTGGAGCCCTCGGTTGAGGCTTTCAGAGAACCTTCCTCGGA 27425

Qy 1066 GGGGAAAAACCGGCTCATGACCCATGATGATGAAACCGGGCGATGCGATCAACCACTCT 1125
 Db 27424 GGGGAAAAACCGGCTCATGACCCATGATGATGAAACCGGGCGATGCGATCAACCACTCT 27365

Qy 1126 GATCAAGGCTTCGAGTCACTCGTGGAGACGAGCTGGAAAAATCGACACTTCTCTC 1185
 Db 27364 GATCAAGGCTTCGAGTTCACCTCGTGGAGACCGCTGGAAAAATCGACACTTCTCTC 27305

Qy 1186 TGMCTTGTGGAGCGAACCTACATGACCGCGTCTTCGGAGTTCGAGACTTCGAGCG 1245
 Db 27304 TGMCTTGTGGAGCGAACCTACATGACCGCGTCTTCGGAGTTCGAGACTTCGAGCG 27245

Qy 1246 GCGGACCGGAACTCTTCATGCGCCACATGCTGGGAGTATGGGCTCATGGAAGCA 1305
 Db 27244 GCGGACCGGAACTCTTCATGCGCCACATGCTGGGAGTATGGGCTCATGGAAGCA 27185

Qy 1306 AGCCGACGAGCGCGCTCTCAGTACAGCTGCAATGTGCGATCAAGTAAACAGCGGGA 1365
 Db 27184 AGCCGACGAGCGCGCTCTCAGTACAGCTGCAATGTGCGATCAAGTAAACAGCGGGA 27125

Qy 1366 CTTGCGAGCTATGAGCGCAAGCTCGCGCGCGGCGAGCGACCAATTAACGGAAAGA 1425
 Db 27124 CTTGCGAGCTATGAGCGCAAGCTCGCGCGCGGCGAGCAACCAATTAACGGAAAGA 27065

Qy 1426 GCTTCTGAGCGCGCGGCTGTCGCGCTCACTCTTCGCTATGAGCTTCAGGAGATGTA 1485
 Db 27064 GCTTCTGAGCGCGCGGCTGTCGCGCTCACTCTTCGCTATGAGCTTCAGGAGATGTA 27005

Qy 1486 GAGGAGGCGAGGCGATGCTCTCCAGCTAGGACATCCCGCGAAATCAGAGATGCGCG 1545
 Db 27004 GAGGAGGCGAGGCGATGCTCTCCAGCTAGGACATCCCGCGAAATCAGAGATGCGCG 26945

Qy 1546 GAGCATATGAGCAITTCGCGAGGTCAGCTGGGATGCGACATTTTCCGACGCTGAA 1605
 Db 26944 GAGCATATGAGCAITTCGCGAGGTCAGCTGGGATGCGACATTTTCCGACGCTGAA 26885

Qy 1606 CCGGACAGGAGAGGCTGCGCGGTAAATAATTGAAACAGCTTCGCGAGCATGGG 1665
 Db 26884 CCGGACAGGAGAGGCTGCGCGGTAAATAATTGAAACAGCTTCGCGAGCATGGG 26825

Qy 1666 CCGGACATATGATGATCGGAGAGATATCGGCGAGGATGATCATATACGCGGA 1725
 Db 26824 CCGGACATATGATGATCGGAGAGATATCGGCGAGGATGATCATATACGCGGA 26765

Qy 1726 GGGGAGACACCTTCAACCAATGAGGCGGCAAGCTTCTAGCATGAGAACTT 1785

Db 26764 GGGGAGACACCTTCAACCAATGAGGCGGCAAGCTTCTAGCATGAGAACTT 26705

Qy 1786 CCGGACGATGCGTGGGAACAACCTTGAAGGCAAGGATGCTTCATGATCAACCG 1845
 Db 26704 CCGGACGATGCGTGGGAACAACCTTGAAGGCAAGGATGCTTCATGATCAACCG 26645

Qy 1846 AGTACTTACTTCCACCGCGTACCTCGATGATCAAGAAAGGCTCAAGCGATCG 1905
 Db 26644 AGTACTTACTTCCACCGCGTACCTCGATGATCAAGAAAGGCTCAAGCGATCG 26585

Qy 1906 GAGCGAGGCTTGAAGGTGTTCATCTCGACCGAGATGAGTACTGCGGATTCATGTT 1965
 Db 26584 GAGCGAGGCTTGAAGGTGTTCATCTCGACCGAGATGAGTACTGCGGATTCATGTT 26525

Qy 1966 TTCCGAGCGACATTCGAAAGAGAGAGTGTGACCGTACTTATGCTTCGACACT 2025
 Db 26524 TTCCGAGCGACATTCGAAAGAGAGAGTGTGACCGTACTTATGCTTCGACACT 26465

Qy 2026 GAGGAGGATTAATGGTGAAGAAAGCTTATGTGCTTGAITGTTGGGCTTGG 2085
 Db 26464 GAGGAGGATTAATGGTGAAGAAAGCTTATGTGCTTGAITGTTGGGCTTGG 26405

Qy 2086 ATTATGTTGCTGCG 2100
 Db 26404 ATTATGTTGCTGCG 26390

RESULT 4
 BK927155/c
 LOCUS BK927155 349136 bp DNA linear 8/14-NOV-2006
 DEFINITION Corynebacterium glutamicum ATCC 13032, IS fingerprint type 4-5, complete genome; segment 8/10.
 ACCESSION BK927155
 VERSION BK927155.1 GI:41326514
 KEYWORDS complete genome.
 SOURCE Corynebacterium glutamicum ATCC 13032
 ORGANISM Corynebacterium glutamicum ATCC 13032
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 REFERENCE 1 (bases 1 to 349136)
 AUTHORS Kalinowski, J., Bathe, B., Bartels, D., Bischoff, N., Bott, M., Burkowski, A., Dusch, N., Eggeling, L., Eikmanns, B. J., Galglat, L., Goesmann, A., Hartmann, M., Huthmacher, K., Kramer, R., Linke, B., McHardy, A. C., Meyer, F., Mook, B., Pfeifferle, W., Puhler, A., Rey, D., Ruckert, C., Rupp, O., Salm, B., Wendisch, V. F., Wiegand, I. and Tauch, A.
 TITLE The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins
 JOURNAL J. Biotechnol. 104 (1-3), 5-25 (2003)
 PUBMED 12948626
 REFERENCE 2 (bases 1 to 349136)
 AUTHORS Kalinowski, J.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer Genomforschung, Universitaet Bielefeld; Universitaetsstrasse 25,